

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 7, 2002, 15:37:26 ; Search time 101.88 Seconds

(without alignments)
462.072 Million cell updates/sec

Title: US-08-569-749-2

Perfect score: 3277

Sequence: 1 MKRTASQRLPFGPSYONIKS.....LRKCPICGILKGTVPFLS 618

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3247	99.1	618	2	S68450 apoptos is inhibito
2	2332	71.2	604	2	S68449 apoptos is inhibito
3	1532	46.8	358	2	JC5964 apoptos is inhibito
4	908	27.7	497	2	S69544 apoptos is inhibito
5	737	22.5	497	2	S69545 apoptos is inhibito
6	723.5	22.1	496	2	S68452 apoptos is inhibito
7	513	15.7	268	2	T10304 inhibitor of apopt
8	513	15.7	268	2	A53989 apoptos is inhibito
9	468	14.3	1447	2	T42628 neuronal apoptos is
10	463	14.1	1232	2	A55478 neuronal apoptos is
11	463	14.1	375	2	A55679 neuronal apoptos is
12	460.5	14.1	398	3	JC7568 kidney inhibitor of
13	240	7.2	992	2	T43523 IAP2 of f22 - Bomby
14	237.5	7.2	286	2	D36828 orf13 protein - Au
15	233.5	6.8	276	2	T10310 apoptos is inhibito
16	223.5	5.9	4845	2	T33067 BIR repeat contain
17	194	5.7	316	2	T32659 hypothetical prote
18	186.5	5.5	711	2	C84767 hypothetical prote
19	181.5	5.4	208	2	T03183 probable apoptos is
20	175.5	5.2	150	2	T28409 Orf MSY246 probabl
21	169	5.0	943	2	S68824 rmgp protein, cyto
22	165	4.9	155	2	T30489 apoptos is inhibito
23	161	4.8	823	2	D86165 protein F15K9.3 (I
24	156	4.6	234	2	T30427 probable apoptos is
25	152	4.6	304	2	T04751 hypothetical prote
26	152	4.6	870	2	G86450 hypothetical prote
27	146	4.4	249	2	H72858 apoptos is inhibito
28	144	4.4	249	2	T41814 IAP2 orf71 - Bomby
29	142	4.3	249	2	T41814

30	140.5	4.3	785	2	T00474 hypothetical prote
31	138	4.2	372	2	C96631 hypothetical prote
32	137.5	4.2	236	2	T10343 inhibitor of apopt
33	137	4.2	614	2	S42526 finger protein unk
34	136.5	4.2	864	2	T01393 apoptos is inhibito
35	135	4.0	899	2	D96594 unknown protein, 7
36	133	4.0	308	2	T37474 apoptos is inhibito
37	130	4.0	115	2	B96664 probable RING zinc
38	129.5	4.0	329	2	T28403 Orf MSY242 probabl
39	128	3.9	247	2	T01044 hypothetical prote
40	126	3.9	1639	2	T50119 probable sensory t
41	126	3.8	145	2	S77736 hypothetical zinc fing
42	124.5	3.8	383	2	F96582 hypothetical prote
43	122	3.7	2364	2	140884 cytoctoxin L - C105
44	121.5	3.7	708	2	T00064 hypothetical prote
45	121.5	3.7	739	2	E86434 protein F17F9.27 1

ALIGNMENTS

RESULT 1
S68450 apoptos is inhibitor hlap-2 - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
C:Accession: S68450
C:History: P.: Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Chertton-Horvat, G.; Faraha
Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by Nalp and a related family of
A:Reference number: A58182; MUID:96149249
A:Accession: S68450
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Features: 1-618 <LIS>
A:Cross-References: EMBL:U45879; NID:91184317; PIDN:MAC50372.1; PID:91184318
A:Function:
C:Description: apoptotic suppressor
C:Superfamily: RING finger homology
C:Keywords: apoptos is; zinc finger
F:567-611/Domain: RING finger homology <RNG>

Query Match	99.1%	Score 3247	DB 2	Length 618
Best local similarity	99.4%	Pred. No. 1.3e-216		
Matches 614	Conservative 0	Mismatches 4	Indels 0	Gaps 0
OY	1	MKRTASQRLPFGPSYONIKS	IMEDSTIISDMTNSNKKMKKYDFSCELYRMSYSTPAGY	60
DB	1	MKRTASQRLPFGPSYONIKS	IMEDSTIISDMTNSNKKMKKYDFSCELYRMSYSTPAGY	60
OY	61	PVSRSLARAGFYTGVDNKKVCFCCGLMDNMKLDSP	IOKHKOLYPSCFTIONLVAS	120
DB	61	PVSRSLARAGFYTGVDNKKVCFCCGLMDNMKLDSP	IOKHKOLYPSCFTIONLVAS	120
OY	121	LSSTSKTSPKNSFAHSLSPTLHSSLSFGSVSLSLP	PLMSRAVEDISSRPNYSVA	180
DB	121	LSSTSKTSPKNSFAHSLSPTLHSSLSFGSVSLSLP	PLMSRAVEDISSRPNYSVA	180
OY	181	MSYSEARLTLYHMPPLTFSSELRAGFYIGPDVAC	FCGCKLSNMPPDDMSH	240
DB	181	MSYSEARLTLYHMPPLTFSSELRAGFYIGPDVAC	FCGCKLSNMPPDDMSH	240
OY	241	RHFPNCPFLNSLETIRFSISLSMOTHAARKMTF	MYSPVPOPLASAGFYVGR	300
DB	241	RHFPNCPFLNSLETIRFSISLSMOTHAARKMTF	MYSPVPOPLASAGFYVGR	300
OY	301	NDVACFCFCCDGLRCWESDDPWVHANRPRCEFL	IRMKGEFYDEIOGRYPHLLQL	360
DB	301	NDVACFCFCCDGLRCWESDDPWVHANRPRCEFL	IRMKGEFYDEIOGRYPHLLQL	360
OY	361	STSDTGTGENADPILHFGPSSSEDAVMNNTPVK	SALENGFNRDLVKOTVOSKILTF	420
DB	361	STSDTGTGENADPILHFGPSSSEDAVMNNTPVK	SALENGFNRDLVKOTVOSKILTF	420

Db 361 STSDTGEENADPPIIHFGPCESSBDPAVMNTPYVKSALKEMLQFNBDLVKQTVLSKILT 420
Oy 421 GENYKTVNDIYVALLNAEDKREKOEKAEEMASDDLILRKNNRMAFLFOOLTCVLTLD 480
Db 421 GENYKTVNDIYVALLNAEDKREKOEKAEEMASDDLILRKNNRMAFLFOOLTCVLTLD 480
Oy 481 NLKANVINKOEHOITKOKTOIPLQARELIDITLVKGNAAANIFKNCJLKEIDSTLYKNLP 540
Db 481 NLKANVINKOEHOITKOKTOIPLQARELIDITLVKGNAAANIFKNCJLKEIDSTLYKNLP 540
Oy 541 VDKNMKYIPTEDVSGLSLEBOLRLQOEPTCKYCKMEKESVYPIFGCHLVYVQCEAPSLR 600
Db 541 VDKNMKYIPTEDVSGLSLEBOLRLQOEPTCKYCKMEKESVYPIFGCHLVYVQCEAPSLR 600
Oy 601 KCPICGIIKGTIVRTFLS 618
Db 601 KCPICGIIKGTIVRTFLS 618

RESULT 2
568449
apoptosis inhibitor hlap-1 - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
C:Accession: S68449
R:Lalston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Parhami,
Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A:Reference number: A58182; MUID:96149249
A:Accession: S68449
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-604 <LIS>
A:Cross-references: EMBL:U45878; NID:g1184315; PIDN:AC03971.1; PID:g1184316
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: RING finger homology
C:Keywords: apoptosis; zinc finger
F:553-597/Domain: RING finger homology <RNG>

Query Match 71.28; Score 2332; DB 2; Length 604;
Best local similarity 72.18; Pred. No. 2,2e-153;
Matches 435; Conservative 72; Mismatches 92; Indels 4; Gaps 4;
Oy 20 SIMEDSTILSDKTNK -HKQAKYDSCELYPMSTYSTEPAQVPSERSLARAGFYTVG 78
Db 2 NIVENSIFLSNLSKANTFELATDLSCELYRSTYSTEPAQVPSERSLARAGFYTVG 61
Oy 79 DAVKCFCCGLMDMMKLGDSPIQKHQLYPSCSFIONLVA -SLGTSKNTSPMRNSFA 136
Db 62 DAVKCFCCGLMDMMKRGDSPTREKHKLYPSCRFVQSLNVNLTATSOPTPSSVTHST 121
Oy 137 HSLSPTLBHSLSFGSYSLSPNPLNSRAVEDISSRTNPFYSAANSTEARFLTYHMP 196
Db 122 HSLSPTEHSGYFSGSYSNSPNSRANQEPALRRSYPCPMKNNAALLTFQWPL 181
Oy 197 TFLSPSELARAGFYIIGPGRVACAFACGKLSNNEPKDAMSEHRHFPNCPFLTENSLE 255
Db 182 TFLSPEDLARAGFYIIGPGRVACAFACGKLSNNEPKDAMSEHRHFPNCPFLTENSLOD 241
Oy 256 TLFESISLSMOTHAARMRTFVWPSSVYVQPEQLASAGFYVYGRNDKFCFCCDGLAR 315
Db 242 TSHYTVSNLSMOTHAARFTKFFWMPSSVYLVNPEQLASAGFYVYGRNDKFCFCCDGLAR 301
Oy 316 MESGDDPMVYHAKKFPCEFLIRKMGSEFVDEIGRYPHILDEQLSTSDTGEENADPPI 375
Db 302 MESGDDPMVYHAKKFPCEFLIRKMGSEFVDEIGRYPHILDEQLSTSDTGEENADPPI 361
Oy 376 IHFGGSESSBDPAVMNTPYVKSALKEMLQFNBDLVKQTVLSKILTGENYKTVNDIYV 435
Db 362 IHFGGSESSBDPAVMNTPYVKSALKEMLQFNBDLVKQTVLSKILTGENYKTVNDIYV 421

Oy 436 NAEDEKREKOEKAEEMASDDLILRKNNRMAFLFOOLTCVLTLDNLKANVINKOEHOI 495
Db 422 NAEDEKREKOEKAEEMASDDLILRKNNRMAFLFOOLTCVLTLDNLKANVINKOEHOI 481
Oy 496 IKOKTOIPLQARELIDITLVKGNAAANIFKNCJLKEIDSTLYKNLPYDKNMKYIPTEDVSG 555
Db 482 IKOKTOIPLQARELIDITLVKGNAAANIFKNCJLKEIDSTLYKNLPYDKNMKYIPTEDVSG 541
Oy 556 LSLBOLRLQOEPTCKYCKMEKESVYPIFGCHLVYVQCEAPSLRKPICGIIKGTIVRT 615
Db 542 LSLBOLRLQOEPTCKYCKMEKESVYPIFGCHLVYVQCEAPSLRKPICGIIKGTIVRT 601
Oy 616 FLS 618
Db 602 FLS 604

RESULT 3
JC5964
apoptosis inhibitor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 02-Sep-2000
C:Accession: JC5964
R:Stehlik, C.; de Martin, R.; Binder, B.R.; Lipp, J.
Biochem. Biophys. Res. Commun. 243, 827-832, 1998
A:Title: Cytokine induced expression of porcine inhibitor of apoptosis protein (Iap)
A:Reference number: JC5964; MUID:98162822
A:Accession: JC5964
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STPE>
A:Cross-references: GB:U79142; NID:92957174; PIDN:AC39171.1; PID:92957175
C:Superfamily: RING finger homology
F:307-351/Domain: RING finger homology <RRN>

Query Match 46.88; Score 1532; DB 2; Length 358;
Best local similarity 65.18; Pred. No. 2e-98; 33; Indels 82; Gaps 2;
Matches 286; Conservative 58; Mismatches 98; Indels 82; Gaps 2;
Oy 181 MSTEENRFLTYHMPFLPSSELARAGFYIIGPGRVACAFACGKLSNNEPKDAMSEH 240
Db 1 MSTEENRFLTYHMPFLPSSELARAGFYIIGPGRVACAFACGKLSNNEPKDAMSEH 60
Oy 241 RHHFPCPELNSL -ETLRPSISLSMOTHAARMRTFVWPSSVYVQPEQLASAGFYTVG 299
Db 61 RHHFPCPELNSL -ETLRPSISLSMOTHAARMRTFVWPSSVYVQPEQLASAGFYTVG 120
Oy 300 RNDVYKCECCGGLRCKWESGDDPMVYHAKKFPCEFLIRKMGSEFVDEIGRYPHILDEQL 359
Db 121 RNDVYKCECCGGLRCKWESGDDPMVYHAKKFPCEFLIRKMGSEFVDEIGRYPHILDEQL 180
Oy 360 LSTSDTGEENADPPIIHFGPCESSBDPAVMNTPYVKSALKEMLQFNBDLVKQTVOSKILT 419
Db 181 LSTSDNPEDENAEPP -NDLSILRKNNRMAFLFOOLTCVLTLD 195
Oy 420 TGENYKTVNDIYVALLNAEDKREKOEKAEEMASDDLILRKNNRMAFLFOOLTCVLTLD 479
Db 196 TGENYKTVNDIYVALLNAEDKREKOEKAEEMASDDLILRKNNRMAFLFOOLTCVLTLD 219
Oy 480 NLKANVINKOEHOITKOKTOIPLQARELIDITLVKGNAAANIFKNCJLKEIDSTLYKNLP 539
Db 220 NLKANVINKOEHOITKOKTOIPLQARELIDITLVKGNAAANIFKNCJLKEIDSTLYKNLP 279
Oy 540 FVDKNMKYIPTEDVSGLSLEBOLRLQOEPTCKYCKMEKESVYPIFGCHLVYVQCEAPSL 599
Db 280 FVDKNMKYIPTEDVSGLSLEBOLRLQOEPTCKYCKMEKESVYPIFGCHLVYVQCEAPSL 339
Oy 600 KCPICGIIKGTIVRTFLS 618
Db 340 KCPICGIIKGTIVRTFLS 358

RESULT 4
 569544
 Apoptosis inhibitor IAP homolog - human
 C:Species: Homo sapiens (man)
 C>Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
 C:Accession: S69544; S68451
 R:Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Giffillan, M.C.
 EMBO J. 15, 2685-2694, 1996
 A:Title: A conserved family of cellular genes related to the baculovirus iap gene and er
 A:Reference number: S69544; MUID:96256286
 A:Accession: S69544
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-497 <DDC>
 A:Cross-references: EMBL:U32974; NID:91016687; PIDN:AC050518.1; PID:91016688
 R:Liston, P.; Roy, N.; Tamai, K.; Letebvre, C.; Baird, S.; Chertton-Horvat, G.; Farhan,
 Nature 379, 349-353, 1996
 A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
 A:Reference number: A58182; MUID:96149249
 A:Accession: S68451
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-161 'C', 163-422, 'Q', 424-497 <LIS>
 A:Cross-references: EMBL:U45880; NID:91164319; PIDN:AC050373.1; PID:91164320
 C:Gene: IIP
 C:Function: IIP
 A:Description: apoptotic suppressor
 C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
 C:Keywords: apoptosis; zinc finger
 F:446-490/Domain: RING finger homology <RRN>

Query Match 27.7%; Score 908; DB 2; Length 497;
 Best Local Similarity 33.8%; Pred. No. 4,4e-53;
 Matches 205; Conservative 88; Mismatches 164; Indels 150; Gaps 14;

QY 35 MKKKMIDSCSELYRMSTYTPAGYVSEKSLARAGFTYTGNDKVKCCGGLMDNKK 94
 DB 18 MKEE--EVEEFNRILTFANFPSSGSPVASTLARAFITGDPYVCFSCGAAADRMQ 74
 QY 95 LGDSPLOKHKQLPSCSFIONLVASLSGSTSKNTSPMRNSF-AHSLSPLEHSLPESGY 153
 DB 75 YGDSAVGRHRYVSPNCRFTINGFYLENSATOSTNSGIONGVKENVLGSRDHFALDRPS- 133
 QY 154 SSLSPNPLNSRAVEDISSRTNPFYSYAMSTEAFRLTYHMP-LFTLSPSLARAGFYI 212
 DB 134 ETRADYLTNGQVYDISDT-IYRNPAMYSEARLKSFOHMPDYAHLTPRELASAGLYYT 192
 QY 213 GPGDRVACFACGKLSHMEPRKDDAMSEHRHFPNCPPL-----EN 252
 DB 193 GIDQVOCFCGCGKIKMEPCDRAWSERHRHFPNCFVLGRNLNLRSSSDAVSSDRNFPN 252
 QY 253 SLETLRFSTLSNMQTHAAMRTFMYWPSYVQPEOLASAGFYVGRNDVKCFCCDGG 312
 DB 253 STYLPR---NSMADYEARIFFPGTWYS--VVKDOLANAGYVAGDEGVKFCRFGGG 306
 QY 313 LRCMESGDDPWYEHAKWFPCEFLIRMKGEFVDEIGRYPHLLD-LLSTSDTTGEEN 371
 DB 307 LTPMKSEBDPMFOHAKWFPCKKYLEOKGOEYINNI--HLSGLEPCVARTTEXT----- 359
 QY 372 DPEIHFPGSESSDEAVMMNTPYVKSALENGPNRDVYKOTYQSKLTTGTENYTVNDY 431
 DB 360 -----PSLTRIDITIFQNPVYOEAIRMGFSKDIKRIKMEKIOISGYSKLEVL 411
 QY 432 SALLNMEDEKREEREKEQAEMASDDLIRKNRMALFOOLTCVPLDNLNKKANVINKO 491
 DB 412 ADLVNKKQDSMPDE----- 425
 QY 492 EHDITKOTQIPIQARELIDITLVKGNMAANIFKNCKLEIDSTLYKNLFPVKNMKYIPT 551
 DB 426 -----SSQTSIQ-----KEI----- 435

QY 552 DVSGLSLEEDLRRLQERTCKYCKMOKESVVFIPCGHLVVCQECAPSLKRCPIRCQIJKG 611
 DB 436 -----STEEQRLRLQGEKCKLCKIDRNIAIVFPCGHLVTCQCAEAVNDKPCWCVITTF 490
 QY 612 TVRFFLS 618
 DB 491 KQKIRMS 497

RESULT 5
 569545
 Apoptosis inhibitor IAP homolog - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
 C:Accession: S69545
 R:Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Giffillan,
 EMBO J. 15, 2685-2694, 1996
 A:Title: A conserved family of cellular genes related to the baculovirus iap gene and
 A:Reference number: S69544; MUID:96256286
 A:Accession: S69545
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-497 <DDC>
 A:Cross-references: EMBL:U32373; NID:91019116; PIDN:AC047155.1; PID:91019117
 C:Gene: IIP
 C:Superfamily: apoptosis inhibitor IAP homolog; RING finger homology
 F:446-490/Domain: RING finger homology <RRN>

Query Match 22.5%; Score 737; DB 2; Length 497;
 Best Local Similarity 30.6%; Pred. No. 2.9e-43;
 Matches 180; Conservative 82; Mismatches 212; Indels 114; Gaps 15;

QY 46 ELRYKSTYTPAGYVSEKSLARAGFTYTGNDKVKCCGGLMDNKKLGDSPTQKXKO 105
 DB 9 ESYRLATGEMPLAAYSAEDLVANGFATGNMLACDFCHVRIDRREVGDOVAAGHR 68
 QY 106 LIPSCSFIONLVASLSGSTSKNTSPMRNSFAHSLSPLEHSLPESGYSSLSPNLSRA 165
 DB 69 SFTCSMY--LAPNHCNVPR-----SQESDNEGNS-- 97
 QY 166 VEDISSRTNPFYSYAMSTEAFRLTYHMP-LFTLSPSLARAGFYIGPDRAVACAGG 225
 DB 98 VVDSPESSCP--DLLEANNRLVTFKDPMPNRTIFQALAKKGFYTLNRKDVKYCWNG 154
 QY 226 KLSNMPKDDAMSEHRHFPNCPPL-----NSLETRETSLSNQH----AA 271
 DB 155 VLAKEKDKNAFEBHKHFPQCRVOMGRLIEPATGKNLDELGLOPTILPLRKRYCYDA 214
 QY 272 RMFTFWPSSVVPQ-EOLASAGFYVGRNDVKCFCCDGGLRCMESGDDPWYEHAKW 330
 DB 215 RLRTFDWPIIS-NIOPASALAOGLYQKIGDOVRCHGCHGKLSMOKEDDPWEHAKMS 273
 QY 331 PRCFLIRMKGEFVDEIGRYPHLLDQLLSTDTTGEENADPPIHFPGSESSDEAVM 390
 DB 274 PKQFVPLAKGPSVSEVLA-----TJNANSSPPT--APAPTLQADVLM 317
 QY 391 MNPVYKSALMGPNRDVYKOTYQSKLTTGTENKYNOIVSALLNMEDEKREEREKEKA 450
 DB 318 DEAP-AKELALGIDGQVYRNALQRLKSSGCAFSITDELHLDID----- 362
 QY 451 EEMASDDLIRKNRMALFOOLTCVPLDNLNKKANVINKOEHDIYKOTQIPIQAREL 510
 DB 363 DACAGADMKCASRPASPF-----IEPCOATYSKA-----ASVPVPAVD 403
 QY 511 DTLVGNMAANIFKNCKLEIDSTLYKNLFPVKNMKYIPTEDVSGLSLEEDLRRLQERT 570
 DB 404 PARPQAEAVANISK-----YDEIOKMSVATPQGNLSLEENROLKDA 449
 QY 571 CKVCMDEKSVVFIPCGHLVVCQECAPSLKRCPIRCQIJKGTVRFFLS 618
 DB 450 CKVCLDEEVGVFLPCGHLATCQCAPYANCPMRADITGIFVETFLS 497

RESULT 6

568452
apoptosis inhibitor diap - fruit fly (*Drosophila melanogaster*)
C|Species: *Drosophila melanogaster*
C|Date: 17-Jul-1998 #sequence_revision 17-Jun-1998 #text_change 17-Nov-2000
C|Accession: S68452; S78528
R|Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Chetron-Horvat, G.; Farahani,
Nature 379, 349-353, 1996
A|Title: Suppression of apoptosis in mammalian cells by NMP and a related family of INH
A|Reference number: A56187; MIMD:95149249
A|Accession: S68452
A|Status: nucleic acid sequence not shown
A|Molecule type: mRNA
A|Residues: 1-496 <LIS>
R|Baird, S.D.
A|Cross-references: EMBL:U45881; MID:g1184313; PIDN:AAC64568.1; PID:g1184314
submitted to the EMBL Data Library, January 1996
A|Reference number: S78528
A|Accession: S78528
A|Molecule type: mRNA
A|Residues: 1-36, AT, .37, 'K', .39, 'L', .41-.44, 'H', .46-.58, 'Q', .60-.412, 'A', .414-.427, 'A', .429-496 <
C|Genetic references: EMBL:045881; MID:g1184313; PIDN:AAC64568.1; PID:g1184314
A|Cross-references: FlyBase:FBN0015247
A|Function:
A|Description: apoptotic suppressor
A|Superfamily: Apoptosis Inhibitor IAP homology; RING finger homology
A|Keywords: apoptosis; zinc finger
A|ZnF:443-489/Domain: RING finger homology <RING>

Query Match	22.1%	Score 723.5:	Db 2:	Length 496:
Best Local Similarity	30.45%	Pred. No. 2.5e-42:		
Matches 180:	Conservative 90:	Mismatches 201:	Indels 119:	Gaps 18:
Qy	46	ELYRNSYTSFFPGVAVSERSLARAQGYTGVNKKVSPCCSGMLMDNKLDDSPDKHKO	105	
Db	9	ESVRLATAFGEMLPAAVSAEDLVANQFQTMW--EADDCPVXRIADHWEYGDCLVAARHRR	66	
Qy	106	LYPSCSFIQWLVSASLSTKSNKSPMRNSFAHLSLPTLRHSLSGSVSLSPPLNRA	165	
Db	67	SSPISQMW--LAPNCGNVPR-----SQSDMEGNS--	95	
Qy	166	VEDSSSNTPYSAVMASTEEARFLTYHMPPLFLPSELARAQGYTIGRGRVACAGG	225	
Db	96	VYDSSECSCP---DLLEANRLVTFKMDPNPNITPOLAKGQFYLRADHYKVCWCG	152	
Qy	226	KLSNNEKDDAMSEHRHHPNCPGLE-----NSLTFEAFSLNLSQTH-----AA	271	
Db	153	VJAKKEKNDAEFEEHRRFFQCPKQMGSLFELFATGNNDLDELQITPLLRPRVACVYA	212	
Qy	272	RHRFPNVPSSVYQD--EQLSAGFYVANDYKCCGCGGIRMGESGDDPWVHAHKKF	330	
Db	213	RIRFTTQMPJLS-NIQPSALAMQGLYKQKISQVYRCHNCIIGLRNKGKEDPEHFAKKS	271	
Qy	331	PACFEILRMKGQFDFEIDQRYPHLLDQLSLSPOTDEEADQPIIHNGPSSSDAYM	390	
Db	272	PQCPQVLLAGRAVYSEV-----LAT--TANMSSQPAF--APAPITQADVLM	315	
Qy	391	KMTVPVSALEKGFQDLKOTYVOSKILTGTGKTYTNDVYSLMLAADEREKEEKKA	450	
Db	316	DEAP--ANEALTLQIDGGVYRNAIDQRKLSSGCASTDELDLHFDQDGAQALFREP	374	
Qy	451	EHMSADSLIRKNRMAFQOLTCVPIIDILLKRAYINKEHDIIKQTOIFL--QARE	508	
Db	375	EPISA-----PIEPQQTTSKASAPPIYVDS-----IFPKQANNE	410	
Qy	509	LIDTILVKGAAANIFKCKLEIDSTLYNNLVFDKNNKTYIPEEDVYSGLSDEQLRLQEE	568	
Db	411	-----ANSNISK-----ITPEDKMSYSTPENGSLSEEBERQJLKA	446	

QY	569	RICKYCMDEKESVYVEIPCGHILVACDSSLRKQIPGIRGIIGTITRFLS	618
	1	:	
Db	447	RICKYCMDEKESVYVEIPCGHILVACDSSLRKQIPGIRGIIGTITRFLS	496
RESULT	7		
	110304		
		Inhibitor of apoptosis protein 3 - <i>Orygia pseudotsugata</i> nuclear polyhedrosis virus	
		C:Species: <i>Orygia pseudotsugata</i> nuclear polyhedrosis virus, <i>Opnnpv</i>	
		C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000	
		C:Accession: T10304	
		C:Authors: G.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Hatwood, S.; Rohmann, G.E.	
		Virology 229, 381-399, 1997	
		A:Title: The sequence of the <i>Orygia pseudotsugata</i> multinucleocapsid nuclear polyhedro	
		A:Reference number: Z10101; M0UD:97271300	
		A:Accession: 110304	
		A:Status: preliminary; translated from GH/EMBL/DBD/J	
		A:Molecule type: DNA	
		A:Residues: 1-268 <NR>	
		A:Cross-references: EMBL/U75930; NID:g2934903; P1DN:AA059034.1; P1D:g1911281	
		A:Superfamily: Viral apoptosis inhibitor JAR; NIM: finger homology	
		/217-261/Domain: finger homology <NR>	

```

Query Match Similarity 15.78; Score 513; DB 2; Length 268;
Best Local Similarity 3.24;18; Pred. No.3,5e-28;
Matches 107; Conservative 51; Mismatches 86; Indels 200; Gaps 4;

OY 181 MSTERARFLYHMMPLETLFSLSPSEIARAGFYIYGQDGVACFCAGCGKLSNNPEKDOMSBN 240
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 15 MNKNAKMLGYTWTMPVOFLSPSRMAASGFYILGDSGDEVRCACXVEITNNVNRDDPEIDH 74
OY 241 RHHNRPDLFENSLSE-----TLFSSISNLSQTLAAARMTFFMYPSSVAPQBPOLAS 292
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 73 KMAHOCDFPRNNADTDPHDAPAPASAAHHQVATAAELTFEMFEMRCLKPAPRELAIE 134
OY 295 AGEFYGRANDYKCFCCDGLRCMESGDDPWEVHAKEKFFPCEFLIRKMGGEFVDEIGRY 352
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 135 AGEFETQDGKTRCFCDCDGLKMEBDQAPMOGHARWYDCIEVYLKYGDFPQR----- 189
OY 353 PHLEBQLLSTSDTQENADPELTHFGPQSSSEDVAVMNTFFYKSALEKGFNRDLVQQT 412
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 190 -----VHTDCAV----- 198
OY 413 VSKRLTTGSKTKYVNDIVSALNAEDKREBEKEXKADEMAASDLSLRKNMALPOOL 472
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 199 -----DQNHETIERVNAE----- 214
OY 473 TQVLEILDNLKANYINKQEHDIKKQKQIPQARLELDIILYKGNMAAMIFKNCLEID 532
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 215 ----- 214
OY 533 STLYKNLFDKMKKTIPTEDVSGISLEBQLRELQEBRTQVCMDEKVSVFIFQGLHYVC 592
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 215 -----VADRLCKTCLGAEKTYCFVDCGHVAC 242
OY 593 OBCAPSLRKCPICRGITKGVATP 616
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 243 GKCAAGVYTCPCVRCQGLDAKAVMY 265

RESULT 8
A53989
apoptosis-inhibiting protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis
C:Species: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OPMNV
C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 15-Sep-2000
C:Accession: A53989
R:Burnbaum, M.J.; Ciem, R.J.; Miller, L.K.
A:Title: An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a po
A:Reference number: A53989; MUID:94187094
A:Accession: A53989.
A>Status: preliminary

```



```

Db      95  IGCFCCLLFLFENGLTRLPRLTDLNKRPHDGGF-----LLAKDGTALVADIRVNN----- 144
Oy      141  PTLHSSLFSGSYSSLSFNNLRNRAVEDISSRPNNYSVAASSTEARFPTLHMP--LTF 198
Db      145  -----LKSRL-----GCKMRY--QEERARLASFANPMPVYGG 175
Oy      199  LSPSELARAGFYIYIGDRAVACACGKLSMPEKPKDAMSEHRRHPNCPFL--ENSLR 255
Db      176  ISPCVLSLEAGVFVTCODTQVCGSCGGCLGMEEGDDPMKDHAKMPKCEFLRASKSSE 235
Oy      256  TLARESIS-----NLNMQT-----NAAKRPFPYMWSSPVQ 286
Db      236  ITQVLYSGKQFDTIGEHFVNSWQRELPMASAYCNDISFAYETELRSLDFSDPMSAVG 295
Oy      287  PEOLASGFYVYGRNDVQKFCDDGGLKWCESDDPPWENAHKMPPCFETLRMGQ--FVY 345
Db      296  VALAKKAGFLPYGIDKIVCGFCGGCLKXNQEDDPLDHHRCPPNCPFLQNMKSSAKYT 355
Oy      346  DEIQGRPHLLFOLLSTSDPTGKBN--ADPPIHFGPSSS--SEDAVMNPNPV----- 395
Db      356  POLGR--GELCELLTETTSSENLSDSIANGPIPYPMAGEAQMGEAKNLNQGLAAATGA 414
Oy      396  -----VKSLE-----NGFNRDLVQVQSGKI--LTGKGYTVNDIVSALNAD 439
Db      415  SFRHSLDITSSDLATDHLGCDLSLASKHISKAPVQPELVLPVFNGLNSVWCCEGASG 474
Oy      440  EKREEREKQAEEMSDSLRKKRMALRQOLTCLP-----LIDNLTK----- 484
Db      475  GKTVLLK--KLARLMSGCGFLNRPQVLFVLSLSTRDEGLASITCDGLERKGSVTBM 533
Oy      485  --AAVINKQENHI--KQKQIPLQARLID-----TLVNGMAANIT--PK 525
Db      534  GMRNIIQGLKNQVFLDDQVKELCISIPQVYSGKLIQNHLNSTGLCLLAVTRRADIRRL 593
Oy      526  NCLKEIDSTLYKN 538
Db      594  ETLEIEQAPFPYN 606

RESULT 11
A:5679
Inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpSV
C:Species: Cydia pomonella granulosis virus GPCV
C:Dates: 21-Sep-1993 #sequence_rev15on 25-Apr-1997 #cexL_change 15-Sep-2000
C:Accession: A45679
R:Cross: N.B.: Clem, R.J.: Miller, L.K.
J:Virol. 67, 2168-2174, 1993
A:Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.
A:Reference number: A45679; NCID:93188158
A:Accession: A45679
A:Status: preliminary
A:Residue type: DNA
A:Residues: 1-275 <CRO>
A:Cross-references: GI:105494; NCBI:q289583; PDB:AAA3935.1; PDB:q289584
A:Note: sequence extracted from NCI backbone (NCBI:127015, NCBI:P127015)
C:Superfamily: Viral apoptosis inhibitor IAP; RING finger homology

Query Match 14.1% Score 461; DB 2; Length 275;
Best Local Similarity 22.6% Pfam NO.1.4e-24;
Matches 103; Conservative 62; Mismatches 84; Indels 206; Gaps 9;

Oy 184  EEARFLTYHMPLETFSPSELARAFYIYIGRGRVACACGKLSMPEKPKDAMSEHRRH 243
Db 7  EEARLNTFKMNVSLSEFLPMANQFITYIGDSVACACVAVELMKKDGEDPAADKKW 66
Oy 244  FPNCPFL-----SLFLTFSLNLSMQTH-----AARRTFMYWSSVP 284
Db 67  APOCLASGFYVYGRNDVQKFCDDGGLKWCESDDPPWENAHKMPPCFETLRMGQ 123
Oy 285  VOPCLASGFYVYGRNDVQKFCDDGGLKWCESDDPPWENAHKMPPCFETLRMGQ 344
:||||: ||||: | | :||| ||||| || | | | :||| | : ||||:

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QY	Db	Query Match	14.1%	Score 460.5	DB 3	Length 298
		Best local similarity	28.8%	Pred. No. 1.9e-24		
		Matches 126	Conservative 36	Mismatches 105	Indels 171	Gaps 13
QY	212	IGPGDPAVACFACGKSLNMEKPKDANSEHRRHFP	---	NC	-----	247
Db	1	MCPRDMSKCHLRQPPSHMAAGDPDVE	---	KCGRSLSGSPVLDLDTCHADHVDQGLIQ	---	58
QY	248	--PLENSLE	---	TLRFSISLNMOTHAARMTFMWPFSSVPVQPOLASAGFYVGR	---	300
Db	59	LRPLTEEEEEEGAGATLSRGPAPFGMSSELRLASFYDMPLTAEVPELLAAAGFRRGH	---	---	---	118
QY	301	NDVYKCFCCDGLKCMWESGDDPVVEYHAKWPRCEFLIRMKGEFVDELQGRPHILLEQL	---	---	---	360
Db	119	QDKRCKEFCVGLQISMKRGDDPMTETAKWPRCQFLRLSRSGRPFVNSVQEN	---	---	---	174
QY	361	STSDTTEENADPPIIHFGPGESSSEDAVMNMTDVYKSALEKGFNRDLVQVQSKILTT	---	---	---	420
Db	175	GSMD	---	PWE-EPDA	---	AVPVSYPASQYPE
QY	421	GENYKTVNDIVSALLMADEKREERKQAEBSMDDLIRKRMALFOOLTCLVPLIID	---	---	---	480
Db	204	---	---	PRRVSSEADBPQGS	---	---
QY	481	NLLKAVINKQEHDIIRKQTOPIQARRELIDTIIIVYKGMAMNIFKCLKLEIDSTLYKNLF	---	---	---	540
Db	221	---	---	PAEQR	---	226

OY 541 VDKNMYIPTEDVSGLSLEBQLRLQERTCKVCNDEKESVVFIPCGHLVWCOBAPSJR 600
 Db 227 -----AMWLEFPGARVDEAQLRLQERTCKVCNDEKESVVFIPCGHLVWCOBAPSJR 280
 OY 601 KCPICGKIGKTVTFELS 618
 Db 281 LCPICRAVPVRSRFTELS 298

RESULT 13

1A1orf127 - Bombyx mori nuclear polyhedrosis virus (isolate T3)
 C:Species: Bombyx mori nuclear polyhedrosis virus, BMSNPV
 A:Variety: Isolate T3
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 15-Sep-2000
 C:Accession: T41772
 R:Gomi, S.; Majima, K.; Maeda, S.
 J. Gen. Virol. 80, 1323-1337, 1999
 A:Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
 A:Reference number: 222020; MID:99281911
 A:Accession: T41772
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-292 <KAM>
 A:Cross-references: EMBL:L31180; NID:g3745835; PIDN:AAC63701.1; PID:g3745854
 A:Experimental source: Isolate T3
 C:Genetics:
 A:Note: 1A1
 C:Superfamily: viral apoptosis inhibitor 1A1; RING finger homology

Query Match 7.3%; Score 240; DB 2; length 292;
 Best Local Similarity 18.0%; Pred. No. 3e-09;
 Matches 78; Conservative 41; Mismatches 96; Indels 218; Gaps 9;
 OY 208 GFTYIGPGDVACFACGKLSNNEPKDAMSEHRHFPNCFLENSLETLPFS----- 260
 Db 54 GFRTYNOVDHVVCEYCEAIKNSSEDCIEVAHTLSFYCAVANKIAEHSFGDNITINA 113
 OY 261 -----ISNLSMOTHAARMKTFM--YNPSSVVPVPEQLASAGFYVVGHPDVK 305
 Db 114 VLVEGRPRKVCYRCKMSNLQ-----SRMDRFVNMFPALRMDITNIAAGLFTGCGDETV 168
 OY 306 CFFCDGGLRCWESGDDPWVEHAKMPFRCFELRMKGQFVVELOIGRPHILLBQLSTSDT 365
 Db 169 CFFCDGGLRCWESGDDPWVEHAKMPFRCFELRMKGQFVVELOIGRPHILLBQLSTSDT 209
 OY 366 TGEENMPRIIHFGSESSSDAVMNTPVVKSALFMGFNDLVKQTVOSKILLTGENTK 425
 Db 210 ----- 209
 OY 426 TVNDIVSALLNADEKREKQAEEMASDLSIRKRMALFOOLLTCVLPILDNLKA 485
 Db 210 -----NAITATTHVDRKDD-----DDD-----DNNTNE 232
 OY 486 NVINKEHDIKOKTOIPLQARELIDTILVKGMAANIFKNCLEIDSTLYKNEFVDKNM 545
 Db 233 NV-----DDDI----- 238
 OY 546 KYIPTEDVSGLSLEBQLRLQERTCKVCNDEKESVVFIPCGHLVWCOBAPSJR-RKCP1 604
 Db 239 -----EKEYECKVCLERQARDVAVLMPCHPCVQVOCYEGSLDCKCP1 278
 OY 605 CPGIKGIVATFL 617
 Db 279 CRQDVATDFIKIFV 291

RESULT 14

T43523
 cut17 protein - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 02-Jun-2000

C:Accession: T43523; T41649; T41700
 R:Morishita, J.; Matsusaka, T.; Yanagida, M.
 Submitted to the EMBL Data Library, August 1999
 A:Description: Fission yeast cut17 is required for chromosome segregation.
 A:Reference number: 222536
 A:Accession: T43523
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-997 <MOR>
 A:Cross-references: EMBL:AB031034; PIDN:BAH83415.1
 R:Harris, D.; Wood, V.; Rajandream, M.A.; Bartell, B.G.
 submitted to the EMBL Data Library, August 1998
 A:Reference number: 222007
 A:Accession: T41649
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-997 <HAR>
 A:Cross-references: EMBL:AL031323; PIDN:CAA20434.1; GSPDB:GNO0068; SPDB:SPCC962.02C
 R:Medler, H.; Duesterhoeft, A.; McDougall, R.C.; Rajandream, M.A.; Bartell, B.G.
 submitted to the EMBL Data Library, October 1999
 A:Reference number: 222010
 A:Accession: T41700
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 932-997 <MED>
 A:Cross-references: EMBL:AL121859; PIDN:CAH58376.1; GSPDB:GNO0068; SPDB:SPCC962.02C
 C:Genetics:
 A:Gene: cut17; SPCC962.02C; SPDB:SPCF31B10.10C
 A:Map position: 3L
 A:Introns: 43/3

Query Match 7.2%; Score 237.5; DB 2; length 997;
 Best Local Similarity 23.1%; Pred. No. 2.7e-08;
 Matches 106; Conservative 63; Mismatches 196; Indels 93; Gaps 22;
 OY 164 RAYEDISSRPNFVSAMSTEARFLTVH--MNPULTFSPSELARAGFY--IGPG---- 215
 Db 2 KPISSSRKRMNFRREKCNYSKRLDTFOKKMPRAKPPETLATVGYNPPISBSSEE 61
 OY 216 --DRVACFACGKLSNNEPKDAMSEHRHFPNCFLENSLETLPFSISNLSMOTHA-- 271
 Db 62 RLDVNTCYMCKTFYVDEDDDLKEHTHSPCPW-----AYILSSNNPNQPAAL 116
 OY 272 ---RMRTFM--YNP-----SSVVPVPEQLASAGFY--VGRNDVYKCCDGGRCMEG 319
 Db 117 TKRGEQFVFKVYPRYNNREDYHCEBSVMAASGFVYNPTRDAKDAHCLYCDIHLHMERD 176
 OY 320 DDPVVEHAKMPFRCFELRMKGQFVDELOIGRPHILL-----QLSTSDTTGEE-NADP 374
 Db 177 DDPTEHRRRADCV-----FTWKDQNSLSTKLSLSTISNIDPDLTEDNS 224
 OY 375 ITHFGSESSSDAVMNTPVVKSALFMGFNDLVKQTVOSK-----IL 418
 Db 225 ILPVSPTFSTKSHATLNFSPSRKNNLAPLMTSLYTTSEKOSQPTAPAPSPKPL 284
 OY 419 TTGENTK-----TVNDIVSALLNADEKREKQAEEMASDLSIRKRNA 467
 Db 285 LTAPRRKRNKPKPKPFAVFKPYKPIFSDEDDDDDLTAQPSKICNDGQVAKN--- 341
 OY 468 LFOQLTCVLPILDNLKANVINKEHDIKOKTOIPLQARELIDTILVKGMAANIFKNC 527
 Db 342 -----FTETIPLEKD-----EKDNELEH--LVSPATSVHTVSDTGHQSVTDESDEQ--NNC 390
 OY 528 LK-----EIDSTLYKNLFPYDKNMKYIPTEDVSGLSLE 560
 Db 391 MSTPKIEIESKIEEIVSVSKSEI--SSVSSVGRQ 427

RESULT 15

D35828
 orf15 protein - Autographa californica nuclear polyhedrosis virus

C:Species: Autographa californica nuclear polyhedrosis virus, ACNMPV
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Nov-2000
C:Accession: D36828; C72853
R:Brünnagel, S.C.; Daniel, K.D.; Rellly, L.M.; Guarino, L.A.; Hong, T.; Summers, M.D.
Virology 191, 1003-1008, 1992
A:Title: Sequence, genomic organization of the EcoRI-A fragment of Autographa californica
VP8 of rotavirus
A:Reference number: A44221; MUID:93079853
A:Accession: D36828
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-286

A:Cross-references: GB:S52569
R:Hayes, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A:Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A:Reference number: A72850; MUID:94303173
A:Accession: C72853
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-199, 'L', 201-286 <AVR>
A:Cross-references: GB:I22858; NID:9510708; PIDN:AAA6657.1; PID:9559096
C:Genetics:
A:Gene: Ac-IAP1
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 7.24; Score 235.5; DB 2; Length 286;
Best Local Similarly 17.64; Pred. No. 5.9e-09;
Matches 83; Conservative 47; Mismatches 112; Indels 229; Gaps 11;

```
OY 173 RTNPSYAMSTEARFLTYHMWPL--TFSPSELRAGFYICGDDRVACACGKLSN 229
DB 18 RDNRTAEHVDMLEIRHNSFENYPIENTAFI--NSLIVNGFKYNOVDHVCYCEAEIKN 75
OY 230 WEPKXDAWSEHRRHFPNCPPLENSLETAFS-----ISNLSMOT 268
DB 76 WSEDECIEEAVHTLSPYCNANKIAERESFGDNITINAVLYKESKRCYKCMNLQ--- 132
OY 269 HAARMETPM-VYPSVYPVQPEOLASAGFYVGRRNDYKCFCCDGLRCHESGDDRWENH 327
DB 133 --SRMDTFVNFPALEMDITNINAGLEITGRGDETVCFCDCCYRDMHTREDWDRHA 190
OY 328 KMFPRCEFLINKGOGEYDEIOGRPHLEBLLSTSDTGTGENADPPIIHFGPGESSSED 387
DB 191 AENRPOCYFVXSVKGRFC----- 208
OY 388 AVNMANTPVVKSALHEGPNRDLVKQTVOSKILTGBENTKTYNDIVSALLMADEKREEKE 447
DB 209 -----ONSITVTNV-----DKRDD-- 222
OY 448 KQAEKASDDLSLRKNRMALFOOLTGVLPIDMLKANYINKOEHDIIKOKTOIPLQAR 507
DB 223 -----DNL-----NENADDI----- 232
OY 508 ELIDTLVKGNAANIFKNCLKEIDSTLVKNLEVDKMKKIPTEDVSGISLEOLRRLOE 567
DB 233 -----EE 234
OY 568 ERTCKVMDKEVSVFIPCGHLVVOECAPSL-RKCPICGRIKGTVRPFL 617
DB 235 KYECKVCLEBRDANVLMPCRHFCVQCIFGLDCKCPTCRQDVTDPRIKIFV 285
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Job time: 701 sec